WHAT IS CLAIMED IS:

1. A method for predicting gene expression sites, comprising:

calculating a distance between first and second genes on a genome sequence, wherein an expression site of the first gene is unknown, and the second gene is one of a plurality of known genes whose expression sites are known; and

determining the expression sites of the first gene based on the distance.

2. The method according to claim 1, wherein

the calculating includes calculating the distance for each of the plurality of genes, and

the determining includes determining the expression sites of the first gene as an expression site of at least one gene that has a predetermined distance relation among the plurality of genes.

3. The method according to claim 1, wherein

the calculating includes calculating a distance between the start position of the first gene and the start position of the second gene on the genome sequence.

4. The method according to claim 1, wherein

the calculating includes calculating a distance between the end position of the first gene and the end position of the second gene on the genome sequence.

5.   The method according to claim 1, wherein

the calculating includes calculating a distance between the start

position of the first gene and the end position of the second gene on the

5   genome sequence.

6.   The method according to claim 1, wherein

the calculating includes calculating a distance between the end

position of the first gene and the start position of the second gene on

10   the genome sequence.

7.   The method according to claim 1, wherein

the calculating includes calculating a distance between first and

second positions, the first position being between the start and end

15   positions of the first gene on the genome sequence, and the second

position being between the start and end positions of the second gene

on the genome sequence.

8.   The method according to claim 1, wherein

20   the calculating includes calculating a distance between a

position between the start and end positions of the first gene and the

start position of the second gene on the genome sequence.

9.   The method according to claim 1, wherein

25   the calculating includes calculating a distance between a

position between the start and end positions of the first gene and the end position of the second gene on the genome sequence.

10.   The method according to claim 1, wherein

5   the calculating includes calculating a distance between the start position of the first gene and a position between the start and end positions of the second gene on the genome sequence.

11.   The method according to claim 1, wherein

10   the calculating includes calculating a distance between the end position of the first gene and a position between the start and end positions of the second gene on the genome sequence.

12.   A method for predicting gene expression sites, comprising:

15   inputting sequence information of a first gene whose expression sites are unknown;

acquiring a position of the first gene in a genome sequence associated with the sequence information;

searching for a second gene whose expression sites are known,

20   the second gene being located around the position of the first gene on the genome sequence;

acquiring information of the expression sites of the second gene;

calculating a distance between the first gene and the second

25   gene on the genome sequence;

sorting a plurality of second genes in ascending order of the

distance; and

outputting the information of the expression sites of the second

gene sorted at the sorting.

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13.   The method according to claim 12, wherein

the outputting includes outputting information of the expression

sites which differs from that of the preceding second gene in the

ascending order.

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14.   The method according to claim 12, further comprising:

displaying a list of the information of the expression sites of the

second gene sorted at the sorting.

15   15.   The method according to claim 12, wherein

the calculating includes calculating a distance between the start

position of the first gene and the start position of the second gene on

the genome sequence.

20   16.   The method according to claim 12, wherein

the calculating includes calculating a distance between the end

position of the first gene and the end position of the second gene on the

genome sequence.

25   17.   The method according to claim 12, wherein

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the calculating includes calculating a distance between the start position of the first gene and the end position of the second gene on the genome sequence.

5   18.   The method according to claim 12, wherein

the calculating includes calculating a distance between the end position of the first gene and the start position of the second gene on the genome sequence.

10   19.   The method according to claim 12, wherein

the calculating includes calculating a distance between first and second positions, the first position being between the start and end positions of the first gene on the genome sequence, and the second position being between the start and end positions of the second gene

15   on the genome sequence.

20.   The method according to claim 12, wherein

the calculating includes calculating a distance between a position between the start and end positions of the first gene and the

20   start position of the second gene on the genome sequence.

21.   The method according to claim 12, wherein

the calculating includes calculating a distance between a position between the start and end positions of the first gene and the

25   end position of the second gene on the genome sequence.

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22.   The method according to claim 12, wherein

       the calculating includes calculating a distance between the start

position of the first gene and a position between the start and end

5   positions of the second gene on the genome sequence.

23.   The method according to claim 12, wherein

       the calculating includes calculating a distance between the end

position of the first gene and a position between the start and end

10   positions of the second gene on the genome sequence.

24.   The method according to claim 12, wherein

       the calculating includes determining a threshold of the distance,

based on a first ratio of a first expression site to expression sites where

15   the unknown gene expresses and a second ratio of a second

expression site to expression sites where the unknown gene does not

express, the first expression site is acquired by the acquiring of

information of the expression sites, and the second expression site is

not acquired by the acquiring of information of the expression sites.

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25.   A computer program product including computer executable

instructions, for predicting gene expression sites, wherein the

instructions, when executed by the computer, cause the computer to

perform:

25   calculating a distance between first and second genes on a

genome sequence, wherein an expression site of the first gene is unknown, and the second gene is one of a plurality of genes whose expression sites are known; and

5   determining the expression sites of the first gene based on the distance.

26.   The computer program product according to claim 25, wherein the determining include determining the expression sites of the first gene as an expression site of at least one gene that has a

10   predetermined distance relation among the plurality of genes.

27.   A computer program product including computer executable instructions, for predicting gene expression, wherein the instructions, when executed by the computer, cause the computer to perform:

15   inputting sequence information of a first gene whose expression site is unknown;

        acquiring a position of the first gene in a genome sequence associated with the sequence information;

        searching for a second gene whose expression sites are known,

20   the second gene being located around the position of the first gene on the genome sequence;

        acquiring information of the expression sites of the second gene;

        calculating a distance between the first gene and the second

25   gene on the genome sequence;

sorting a plurality of second genes in ascending order of the distance; and

outputting the information of the expression sites of the second gene sorted at the sorting.

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28.   An apparatus for predicting gene expression, comprising:

a calculation unit that calculates a distance between first and second genes on a genome sequence, wherein an expression site of the first gene is unknown, and the second gene is one of a plurality of

10   genes whose expression sites are known; and

a determination unit that determines the expression sites of the first gene based on the distance.

29.   The apparatus according to claim 28, wherein

15   the calculation unit calculates the distance for each of the plurality of genes, and

the determination unit determines the expression sites of the first gene as an expression site of at least one gene that has a predetermined distance relation among the plurality of genes.

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30.   An apparatus for predicting gene expression sites, comprising:

an input unit to input sequence information of a first gene whose expression site is unknown;

a positional information acquisition unit that acquires a position

25   of the first gene in a genome sequence associated with the sequence

information;

a searching unit that searches for a second gene whose expression sites are known, the second gene being located around the position of the first gene on the genome sequence;

5   an expression site information acquisition unit that acquires information of the expression sites of the second gene;

a calculation unit that calculates a distance between the first gene and the second gene on the genome sequence;

a storage unit that stores a plurality of second genes in

10 ascending order of the distance; and

an output unit that outputs the information of the expression sites of the second gene sorted by the storage unit.